

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bartley, Timothy D.  
Bogenberger, Jakob M.  
Bosselman, Robert A.  
Hunt, Pamela  
Samal, Babru B.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR STIMULATING  
MEGAKARYOCYTE GROWTH AND DIFFERENTIATION
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Amgen Inc.  
(B) STREET: 1840 Dehavilland Drive  
(C) CITY: Thousand Oaks  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/347,780  
(B) FILING DATE: 30-NOV-1994  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/252,628  
(B) FILING DATE: 31-MAY-1994
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/221,768  
(B) FILING DATE: 31-MAR-1994
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/321,488  
(B) FILING DATE: 12-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Cook, Robert R.  
(B) REGISTRATION NUMBER: 31,602  
(C) REFERENCE/DOCKET NUMBER: A-290C

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Pro	Pro	Ala	Xaa	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Met	Leu	Arg	Asp
1				5					10					15	
Ser	His	Val	Leu	His	Xaa	Arg	Leu	Xaa	Gln	Xaa	Pro	Asp	Ile	Tyr	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
1 5 10 15  
Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala  
1 5 10 15  
Leu

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCNCCNCCNG CNTGYGA

17

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*C13*  
*cont.* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCARTGYAAC ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp  
1 5 10 15  
Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTACGCGTTC TAGANNNNNN T

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTTTACTGA GGACTCGGAG G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

C13  
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGACCTCC GAGTCCTCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTCCTCAG TAAACTGCTT CGT

23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGTCACGA AGCAGTTTAC

20

C<sup>13</sup>  
cont.

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTTTACTTC TAGGCCTG

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGTCACAA GCAGGAGGA

19

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCATAGTCC GGGACGTCG

19

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCTCCTGCT TGTGACCTC

19

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGGAAGGA TTCAGGGGA

19

(2) INFORMATION FOR SEQ ID NO:19:

- C13  
cont.
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAACAAGTCG ACCGCCAGCC AGACACCCCG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGGATAG GCCACTCNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCARTGYAAN ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGTGTGCA CTTGTG

16

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACAAGTGCA CACCAACCCC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1342 base pairs

C13  
cont.



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 36..1097

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 99..1097

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 36..98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGAGCCA CGCCAGCCAA GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG	53
Met Glu Leu Thr Glu Leu	
-21 -20	
CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC	101
Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser	
-15 -10 -5 1	
CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT	149
Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg	
5 10 15	
GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC	197
Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His	
20 25 30	
CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA	245
Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly	
35 40 45	
GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA	293
Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly	
50 55 60 65	
GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG	341
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu	
70 75 80	
GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC	389
Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val	
85 90 95	
CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT	437
Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro	
100 105 110	

C B  
cont.

CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG 485  
Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu  
115 120 125

AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA 533  
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val  
130 135 140 145

GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC 581  
Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val  
150 155 160

CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG AAC GAG CTC CCA AAC AGG 629  
Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg  
165 170 175

ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT 677  
Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr  
180 185 190

GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT CCT 725  
Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro  
195 200 205

GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA ATC CCC GGA TAC 773  
Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr  
210 215 220 225

CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA ACT CGT GGA CTC TTT CCT 821  
Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro  
230 235 240

GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA 869  
Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr  
245 250 255

TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 917  
Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro  
260 265 270

TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC CCT CTT CCA 965  
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro  
275 280 285

CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC CAC CCC CTG CTT CCT GAC 1013  
Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro Asp  
290 295 300 305

CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC CCT CTT CTA AAC ACA TCC 1061  
Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser  
310 315 320

TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA GGG TAA GGTTCTCAGA 1107  
Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly \*

CACTGCCGAC ATCAGCATTG TCTCGTGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA 1167

C13  
cont.

GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA AAAGGGATAC 1227  
 ACAGGACTGA AAAGGGAATC ATTTTTCAC TACATTATA AACCTTCAGA AGCTATTTTTT 1287  
 TTAAGCTATC AGCAATACTC ATCAGAGCAG CTAGCTCTTT GGTCTATTTT CTGCA 1342

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala  
 -21 -20 -15 -10  
 Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val  
 -5 1 5 10  
 Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
 15 20 25  
 Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
 30 35 40  
 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
 45 50 55  
 Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
 60 65 70 75  
 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
 80 85 90  
 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
 95 100 105  
 Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
 110 115 120  
 Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 125 130 135  
 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
 140 145 150 155  
 Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
 160 165 170  
 Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
 175 180 185

C3  
 cont.

Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
190 195 200

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
220 225 230 235

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
240 245 250

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
255 260 265

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
270 275 280

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
285 290 295

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
300 305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
320 325 330

Gly \*

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGGAGCCAC GCCAGCCAGA CACCCCGGCC AGAATGGAGC TGA	60
CTGCTCCTGCTC TCCTAACTGC AAGGCTAACG CTGTCC AGC	114
CCG GCT CCT CCT GCT	
Ser Pro Ala Pro Pro Ala	
1 5	
TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT	162
Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu	
10 15 20	

C13  
cont.

CAC	AGC	AGA	CTG	AGC	CAG	TGC	CCA	GAG	GTT	CAC	CCT	TTG	CCT	ACA	CCT	210
His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	
	25						30					35				
GTC	CTG	CTG	CCT	GCT	GTG	GAC	TTT	AGC	TTG	GGA	GAA	TGG	AAA	ACC	CAG	258
Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	
	40					45					50					
ATG	GAG	GAG	ACC	AAG	GCA	CAG	GAC	ATT	CTG	GGA	GCA	GTG	ACC	CTT	CTG	306
Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	
55					60					65					70	
CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	354
Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	
				75					80					85		
TCA	TCC	CTC	CTG	GGG	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	GGG	402
Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	
			90					95					100			
GCC	CTG	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	ACC	450
Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	
	105						110					115				
ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	TTC	CAA	CAC	CTG	498
Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	
	120					125					130					
CTC	CGA	GGA	AAG	GAC	TTC	TGG	ATT	GTT	GGA	GAC	AAA	CTT	CAC	TGC	CTC	546
Leu	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp	Lys	Leu	His	Cys	Leu	
135					140					145					150	
AGC	CAG	AAC	TAC	TGG	CTC	TGG	GCT	TCT	GAA	GTG	GCA	GCA	GGG	ATT	CAG	594
Ser	Gln	Asn	Tyr	Trp	Leu	Trp	Ala	Ser	Glu	Val	Ala	Ala	Gly	Ile	Gln	
				155					160					165		
AGC	CAA	GAT	TCC	TGG	TCT	GCT	GAA	CCA	AAC	CTC	CAG	GTC	CCT	GGA	CCA	642
Ser	Gln	Asp	Ser	Trp	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Val	Pro	Gly	Pro	
			170					175					180			
AAT	CCC	CGG	ATA	CCT	GAA	CAG	GAT	ACA	CGA	ACT	CTT	GAA	TGG	AAC	TCG	690
Asn	Pro	Arg	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Leu	Glu	Trp	Asn	Ser	
	185						190					195				
TGG	ACT	CTT	TCC	TGG	ACC	CTC	ACG	CAG	GAC	CCT	AGG	AGC	CCC	GGA	CAT	738
Trp	Thr	Leu	Ser	Trp	Thr	Leu	Thr	Gln	Asp	Pro	Arg	Ser	Pro	Gly	His	
	200					205					210					
TTC	CTC	AGG	AAC	ATC	AGA	CAC	AGG	CTC	CCT	GCC	ACC	CAA	CCT	CCA	GCC	786
Phe	Leu	Arg	Asn	Ile	Arg	His	Arg	Leu	Pro	Ala	Thr	Gln	Pro	Pro	Ala	
215					220					225					230	
TGG	ATA	TTC	TCC	TTC	CCC	AAC	CCA	TCC	TCC	TAC	TGG	ACA	GTA	TAC	GCT	834
Trp	Ile	Phe	Ser	Phe	Pro	Asn	Pro	Ser	Ser	Tyr	Trp	Thr	Val	Tyr	Ala	
				235					240					245		

C13  
cont.

CTT CCC TCT TCC ACC CAC CTT GCC CAC CCC TGT GGT CCA GCT CCA CCC	882
Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro Ala Pro Pro	
250 255 260	
CCT GCT TCC TGACCCTTCT GCTCCAACGC CCACCCCTAC CAGCCCTCTT	931
Pro Ala Ser	
265	
CTAAACACAT CCTACACCCA CTCCCAGAAAT CTGTCTCAGG AAGGGTAAGG TTCTCAGACA	991
CTGCCGACAT CAGCATTGTC TCGTGTACAG CTCCCTTCCC TGCAGGGCGC CCCTGGGAGA	1051
CAACTGGACA AGATTTCTCTA CTTTCTCCTG AAACCCAAAG CCCTGGTAAA AGGGATACAC	1111
AGGACTGAAA AGGGAATCAT TTTTCACTGT ACATTATAAA CCTTCAGAAG CTA	1164

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

C13  
cont.

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu
1				5					10					15	
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val
			20					25					30		
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu
			35				40					45			
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu
	50					55					60				
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln
	65				70				75						80
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln
				85				90						95	
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu
			100					105					110		
Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe
			115				120					125			
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly
	130					135					140				
Asp	Lys	Leu	His	Cys	Leu	Ser	Gln	Asn	Tyr	Trp	Leu	Trp	Ala	Ser	Glu
145					150				155						160

Val Ala Ala Gly Ile Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn  
165 170 175

Leu Gln Val Pro Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg  
180 185 190

Thr Leu Glu Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp  
195 200 205

Pro Arg Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro  
210 215 220

Ala Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser  
225 230 235 240

Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro  
245 250 255

Cys Gly Pro Ala Pro Pro Pro Ala Ser  
260 265

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..498

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 7..498

- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG AAA AGT CCT GCA CCA CCT GCA TGT GAT TTA CGG GTC CTG TCT AAA	48
Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys	
-2 1 5 10	
CTG CTG CGC GAC TCT CAC GTG CTG CAC TCT CGT CTG TCC CAG TGC CCG	96
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro	
15 20 25 30	
GAA GTT CAC CCG CTG CCG ACC CCG GTT CTG CTT CCG GCT GTC GAC TTC	144
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe	
35 40 45	

C13  
wt.

C13  
cont.

TCC CTG GGT GAA TGG AAA ACC CAG ATG GAA GAG ACC AAA GCT CAG GAC	192
Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp	
50 55 60	
ATC CTG GGT GCA GTA ACT CTG CTT CTG GAA GGC GTT ATG GCT GCA CGT	240
Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg	
65 70 75	
GGC CAG CTT GGC CCG ACC TGC CTG TCT TCC CTG CTT GGC CAG CTG TCT	288
Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser	
80 85 90	
GGC CAG GTT CGT CTG CTG CTC GGC GCT CTG CAG TCT CTG CTT GGC ACC	336
Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr	
95 100 105 110	
CAG CTG CCG CCA CAG GGC CGT ACC ACT GCT CAC AAG GAT CCG AAC GCT	384
Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala	
115 120 125	
ATC TTC CTG TCT TTC CAG CAC CTG CTG CGT GGC AAA GTT CGT TTC CTG	432
Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu	
130 135 140	
ATG CTG GTT GGC GGT TCT ACC CTG TGC GTT CGT CGG GCG CCG CCA ACC	480
Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr	
145 150 155	
ACT GCT GTT CCG TCT TAA	498
Thr Ala Val Pro Ser *	
160	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys	
-2 1 5 10	
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro	
15 20 25 30	
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe	
35 40 45	
Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp	
50 55 60	



Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg  
65 70 75

Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser  
80 85 90

Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr  
95 100 105 110

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala  
115 120 125

Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu  
130 135 140

Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr  
145 150 155

Thr Ala Val Pro Ser \*

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCAGGTCG AACTAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:

C13  
cont.

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCATAATTT TTAAAAAATT CATTTGACAA ATGCTAAAAT TCTTGATTAA TATTCTCAAT 60  
TGTGAGCGCT CACAATTTAT 80

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 86 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

C<sup>13</sup>  
ord.  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGATAAATTG TGAGCGCTCA CAATTGAGAA TATTAATCAA GAATTTTAGC ATTTGTCAAA 60  
TGAATTTTTT AAAAATTATG AGACGT 86

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACGTCTCAT AATTTTTTAAA AAATTCATTT GACAAATGCT AAAATTCCTG ATTAATATTC 60  
TCAATTGTGA GCGCTCACAA TTTATCGAT 89